

EXHIBIT 7



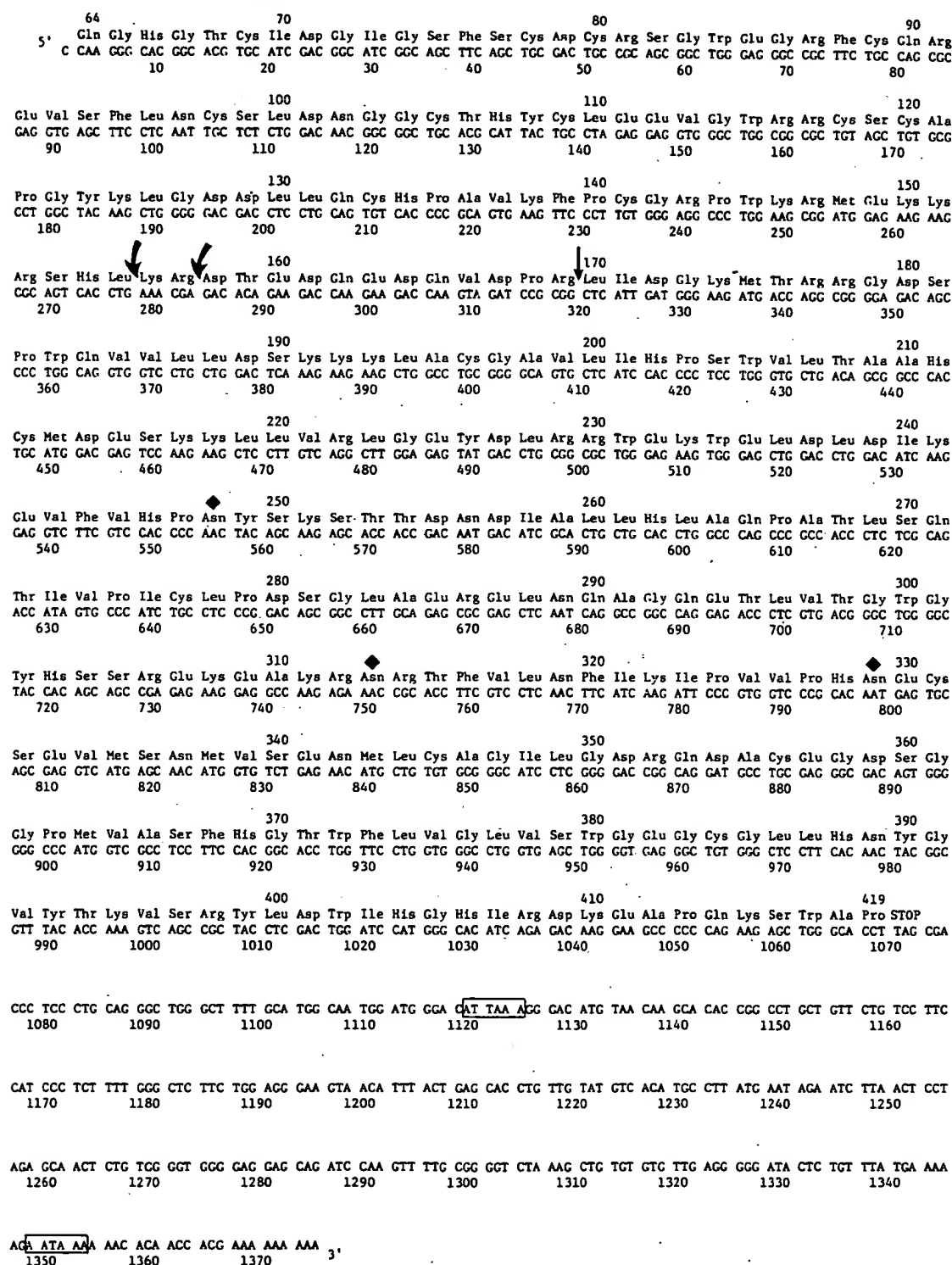


FIG. 2. Nucleotide sequence of the cDNA inserts in λ HC1026 and λ HC1375 that code for human protein C. The predicted amino acid sequence is shown starting with residue 64 in the light chain. This numbering assumes that the length of the light chain of bovine and human protein C is identical. ♦, Potential carbohydrate binding sites to asparagine residues; ↓, apparent cleavage sites for removal of the connecting dipeptide; |, site of cleavage in the heavy chain when protein C is converted to activated protein C; ●, site of polyadenylation in λ HC1026. The processing or polyadenylation sequences are shown in boxes.

pears to be one of the few serine proteases that has a leucine rather than an isoleucine or valine in this position.

The nucleotide sequences near the active-site serine for protein C and three other human vitamin K-dependent serine protease cDNAs (25, 34–36) are shown in Fig. 4. DNA and amino acid sequence homology in this region is highly con-

served. The cDNAs isolated in this investigation lack the 5' end. This region codes for approximately 63 additional amino acids present in the light chain and a leader sequence that is typical of secreted proteins (37). It should be of interest to compare the DNA sequence corresponding to this region of protein C with factor IX and factor X, since these three pro-